SEQUENCE LISTING

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(1) GENERAL INFORMATION:

(i) APPLICANT!

(A) NAME: \NOVO NORDISK A/S

(B) STREET Novo Alle (C) CITY: DK-2880 Bagsvaerd

(E) COUNTRY Denmark (F) POSTAL CODE (ZIP): DK-2880

(G) TELEPHONE: +45 44 44 88 88 (H) TELEFAX: +45 44 49 32 56

(ii) TITLE OF INVENTION: a-amylase variants

(iii) NUMBER OF SEQUENCES: 32

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

## (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTER STICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: proteit
- (iii)Organism: Bacillus sp.\ (xi) SEQUENCE DESCRIPTION: \$EQ ID NO: 1:

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp

Leu Pro Asn Asp Gly Asn His Ttp Asn Arg Leu Arg Asp Asp Ala Ala

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr

Asp Leu Gly Glu Phe Asn Cln Lys Gly Thr Val Arg Thr Lys Tyr Gly

Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn 50

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met 65

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	Asp	His 210	Pro	Glu	Val	Ile	His 215	Glu	Leu	Arg	Asn	Trp 220	Gly	Val	Trp	Tyr
5	Thr 225	Asn	Thr	Leu	Asn	Leu 230	Asp	Gly	Phe	Arg	Ile 235	Asp	Ala	Val	Lys	His 240
	Ile	Lys	Tyr	Ser	Phe 245	Thr	Arg	Asp	Trp	Leu 250	Thr	His	Val	Arg	Asn 255	Thr
10	Thr	Gly	Lys	Pro 260	Met	Phe	Ala	Val	Ala 265	Glu	Phe	Trp	ГÀЗ	Asn 270	Asp	Leu
15	Gly	Ala	Ile 27 <b>5</b>	Glu	Asn	Tyr	Leu	Asn 200	Lys	Thr	Ser	Trp	Asn 285	His	Ser	Val
	Phe	Asp 290	Val	Pro	Leu	His	Tyr 295	Asn	Leu	Tyr	Asn	Ala 300	Ser	Asn	Ser	Gly
20	Gly 305	Tyr	Tyr	Asp	Met	Arg 310	Asn	Ile	Leu	Asn	Gly 315	Ser	Val	Val	Gln	Lys 320
	His	Pro	Thr	His	Ala 325	Val	Thr	Phe	Val	Asp 330	Asn	His	Asp	Ser	Gln 335	Pro
= 25 = = = = = = = = = = = = = = = = = = =	Gly	Glu	Ala	Leu 340	Glu	ser	Phe	Val	Gln 345	Gln	Trp	Phe	Lys	Pro 350	Leu	Ala
1430	Туг	Ala	Leu 355	Val	Leu	Thr	Arg	Glu 360	Gln	Gly	Tyr	Pro	Ser 365	Val	Phe	Tyr
	Gly	Asp 370	Tyr	Tyr	Gly	Ile	Pro 375	Thr	His	Gly	Val	Pro 380	Ala	Met	ŗňa	Ser
:  35 	Lys 385	Ile	qaA	Pro	Leu	Leu 390	Gln	Ala	Arg	Gln	Thr 395	Phe	Ala	Tyr	Gly	Thr 400
	Gln	His	Asp	Tyr	Phe 405	Asp	His	His	Asp	Ile 410	Ile	Gly	Trp	Thr	Arg 415	Glu
140 11	Gly	Asn	Ser	Ser 420	His	Pro	Asn	Ser	Gly 425	Leu	Ala	Thr	Ile	Met 430	Ser	Asp
45		Pro	435					440					445			_
		Val 450					455					460				
50	Asn 465	Ala	Asp	Gly	Trp	Gly 470	Asn	Phe	Ser	Val	Asn 475	Gly	Gly	Ser	Val	Ser 480
	Val	Trp	Val	Lys	Gln 485											
55	(2) INFOI (i)	SEQU (A) (B)	JENCE LEN TYL		RACT 485	ERIS ami aci	TICS .no a .d	: cids	ŀ							
60	(ii) (iii) (xi) SEQU	(D) MOLE Orga	TOI CULE nisn	POLOG E TYE n: Ba	Y: l E: p cill	inea rote us s	ir in sp.		2:							
65	His 1	His	Asn	Gly	Thr 5	Азп	Gly	Thr	Met	Мет 10	Gln	Tyr	Phe	Glu	Trp 15	His

	Lev	Pro	Asn	Asp 20	Gly	Asn	His	Trp	Asn 25	Arg	Leu	Arg	Asp	Asp 30	Ala	Ser
5	Asr	Leu	Arg 35	Asn	Arg	Gly	Ile	Thr 40	Ala	Ile	Trp	Ile	Pro 45	Pro	Ala	Trp
	Lys	Gly 50	Thr	Ser	Gln	Aen	Asp 55	Val	Gly	Tyr	Gly	Ala 60	Tyr	Asp	Leu	Tyr
10	Asp 65	Leu	Gly	Glu	Phe	Asn 70	Gln	Lys	Gly	Thr	Val 75	Arg	Thr	Lys	Tyr	Gly 80
15	Thr	Arg	Ser	Gln	Leu 85	Glu	Ser	Ala	Ile	His 90	Ala	Leu	Lys	Asn	Asn 95	Gly
13	Val	Gln	Val	Tyr 100	Gly	Asp	Val	Val	Met 105	Asn	His	Lys	Gly	Gly 110	Ala	Asp
20	Ala	Thr	Glu 115	Aen	Val	Leu	Ala	Val 120	Glu	Val	Asn	Pro	Asn 125	Asn	Arg	Asn
T T	Gln	Glu 130	Ile	Ser	Gly	Asp	Tyr 135	Thr	Ile	Glu	Ala	Trp 140	Thr	Lys	Phe	Asp
===25	Phe 145	Pro	Gly	Arg	Gly	Asn 150	Thr	Tyr	Ser	qzA	Phe 155	Lys	Trp	Arg	Trp	Tyr 160
-   <u> </u>  -30	His	Ph∉	Asp	Gly	Val 165	Asp	Trp	Asp	Gln	Ser 170	Arg	Gln	Phe	Gln	Asn 175	Arg
IJ	Ile	Tyr	Lys	Phe 180	Arg	Gly	Asp	Gly	Lys 185	Ala	Trp	Asp	Trp	Glu 190	Val	Asp
  -35	Ser	Glu	Asn 195	Gly	Asn	Tyr	Asp	Tyr 200	Leu	Met	Tyr	Ala	Asp 205	Val	Asp	Met
	Asp	His 210	Pro	Glu	Val	Val	Asn 215	Glu	Leu	Arg	Arg	Trp 220	Gly	Glu	Trp	Tyr
Lo	Thr 225	Asn	Thr	Leu	Asn	Leu 230	Asp	Gly	Phe	Arg	Ile 235	Asp	Ala	Val	Lys	His 240
45	Ile	Lys	Tyr	Ser	Phe 245	Thr	Arg	Asp	Trp	Leu 250	Thr	His	Val	Arg	Asn 255	Ala
43	Thr	Gly	Lys	Glu 260	Met	Phe	Ala	Va1	Ala 265	Glu	Phe	Trp	Lys	Asn 270	Asp	Leu
50	Gly	Ala	Leu 275	Glu	Asn	Tyr	Leu	Asn 280	Lys	Thr	Asn	Trp	Asn 285	His	Ser	Val
	Phe	Asp 290	Val	Pro	Leu	His	Tyr 295	Asn	Leu	Tyr	Asn	Ala 300	Ser	Asn	Ser	Gly
55	Gly <b>30</b> 5	Asn	Tyr	qaA	Met	Ala 310	Lys	Leu	Leu	Asn	Gly 315	Thr	Val	Val	Gln	Lys 320
60	His	Pro	Met	His	Ala 325	Val	Thr	Phe	Val	Asp 330	Asn	His	Asp	Ser	Gln 335	Pro
60	Gly	Glu	Ser	Leu 340	Glu	Ser	Phe	Val	Gln 345	Glu	Trp	Phe	Lys	Pro 350	Leu	Ala
65	Tyr	Ala	Leu 355	Ile	Leu	Thr	Arg	Glu 360	Gln	Gly	Тут	Pro	Ser 365	Val	Phe	Tyr
	Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Ser	Val	Pro	Ala	Met	Lys	Ala

370 375 380 Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr 390 5 Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu 410 Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp 10 425 Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile 15 Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser 20 Ile Trp Val Lys Arg IJ ٠D (2) INFORMATION FOR SEQ ID NO: 3: - -25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 514 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear إيا (ii) MOLECULE TYPE: protein 30 (iii) Organism: Bacillus stearothermophilus. Ш (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: # Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu ŀ÷ 35 ļ. Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn 20 25 30 1= m 40 Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys ũ Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp 50 55 45 Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr 65 70 80 Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met 50 Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln 55 Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe 60 Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr 65 Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu

					190					185					190		
	5	Asn	Gly	Asn 195	Tyr	Asp	Tyr	Leu	Met 200	Tyr	Ala	Asp	Leu	Asp 205		Asp	His
		Pro	Glu 210	Val	Val	Thr	Glu	Leu 215	Lys	Ser	Trp	Gly	Lys 220	Trp	Tyr	Val	Asn
	10	Thr 225	Thr	Asn	Ile	Asp	Gly 230	Phe	Arg	Leu	Asp	Ala 235	Val	Lys	His	Ile	Lув 240
		Phe	Ser	Phe	Phe	Pro 245	Asp	Trp	Leu	Ser	Asp 250	Val	Arg	Ser	Gln	Thr 255	Gly
	15	Lys	Pro	Leu	Phe 260	Thr	Val	Gly	Glu	Tyr 265	Trp	Ser	Tyr	Asp	Ile 270	Asn	Lys
	20	Leu	His	Asn 275	Tyr	Ile	Met	Lys	Thr 280	Asn	Gly	Thr	Met	Ser 205	Leu	Phe	Asp
	20	Ala	Pro 290	Leu	His	Asn	Lys	Phe 295	Tyr	Thr	Ala	Ser	Lys 300	Ser	Gly	Gly	Thr
	25	Phe 305	Asp	Met	Arg	Thr	Leu 310	Met	Thr	Asn	Thr	Leu 315	Met	Lys	Asp	Gln	Pro 320
T W		Thr	Leu	Ala	Val	Thr 325	Phe	Val	Asp	Asn	His 330	Asp	Thr	Glu	Pro	Gly 335	Gln
	30	Ala	Leu	Gln	Ser 340	Trp	Val	Asp	Pro	Trp 345	Phe	Lys	Pro	Leu	Ala 350	Tyr	Ala
		Phe	Ile	Leu 355	Thr	Arg	Gln	Glu	Gly 360	Tyr	Pro	Cys	Val	Phe 365	Tyr	Gly	Asp
	•	Tyr	Tyr 370	Gly	Ile	Pro	Gln	Tyr 375	Asn	Ile	Pro	Ser	Leu 380	Lys	Ser	Lye	Ile
	40	Asp 385	Pro	Leu	Leu	Ile	Ala 390	Arg	Arg	Asp	Tyr	Ala 395	Tyr	Gly	Thr	Gln	His 400
* Har		qaA	Tyr	Leu	Asp	His 405	Ser	Asp	Ile	Ile	Gly 410	Trp	Thr	Arg	Glu	Gly 415	Val
4	ł S	Thr	Glu	Lys	Pro 420	Gly	Ser	Gly	Leu	Ala 425	Ala	Leu	Ile	Thr	Asp 430	Gly	Pro
	50	Gly	Gly	Ser 435	ГÀЗ	Trp	Met	Tyr	Val 440	Gly	Lys	Gln	His	Ala 445	Gly	Lys	Val
-		Phe	Tyr 450	Asp	Leu	Thr	Gly	Asn 455	Arg	Ser	Asp	Thr	Val 460	Thr	Ile	Asn	Ser
9	55	Asp 465	Gly	Trp	Gly	Glu	Phe 470	Lys	Val	Asn	Gly	Gly 475	Ser	Val	Ser	Val	Trp 400
		Val	Pro	Arg	Lуз	Thr 485	Thr	Val	Ser	Thr	Ile 490	Ala	Trp	Ser	Ile	Thr 495	Thr
6	60	Arg	Pro	Trp	Thr 500	Asp	Glu	Phe	Val	Arg 505	Trp	Thr	Glu	Pro	Arg 510	Leu	Val
		Ala	Trp														

(2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 483 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein

(iii) Organism: Bacillus licheniformis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro 10 1 5 10 15

Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu 20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu 50 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn 85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro 130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe 145 150 150

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys 165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn 180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val 195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln 210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe 225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met 245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn 260 265 270

60 Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu 275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Tyr Asp Met 290 295

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser 305 310 320

		Val	Thr	Phe	Val	Asp 325	Asn	His	Asp	Thr	Gln 330	Pro	Gly	Gln	Ser	Leu 335	Glu
. 5		Ser	Thr	Val	Gln 340	Thr	Trp	Phe	Lys	Pro 345	Leu	Ala	Tyr	Ala	Phe	Ile	Leu
		Thr	Arg	Glu 355	Ser	Gly	Tyr	Pro	Gln 360	Val	Phe	Tyr	Gly	Asp 365	Met	Tyr	Gly
10		Thr	Lys 370	Gly	Asp	Ser	Gln	Arg 375	Glu	Ile	Pro	Ala	Leu 380	ГÀа	His	Lys	Ile
15		Glu 385	Pro	Ile	Leu	Lys	Ala 390	Arg	Lys	Gln	Tyr	Ala 395	Tyr	Gly	Ala	Gln	His 400
		Asp	Tyr	Phe	Asp	His 405	His	Asp	Ile	Val	Gly 410	Trp	Thr	Arg	Glu	Gly 415	Asp
20		Ser	Ser	Val	Ala 420	Asn	Ser	Gly	Leu	Ala 425	Ala	Leu	Ile	Thr	Asp 430	Gly	Pro
		Gly	Gly	Ala 435	Lys	Arg	Met	Tyr	Val 440	Gly	Arg	Gln	Asn	Ala 445	Gly	Glu	Thr
- 25 - 25 - 1		Trp	His 450	Asp	Ile	Thr	Gly	Asn 455	Arg	Ser	Glu	Pro	Val 460	Val	Ile	Asn.	Ser
1. <u>1</u> 30		Glu 465	Gly	Trp	Gly	Glu	Phe <b>4</b> 70	His	Val	Asn	Gly	Gly 475	Ser	Val	Ser	Ile	Tyr 480
		Val	Gln	Arg													
£																	
35	- (	(i) (ii) (iii)	(B)	JENCE LEN TYE STE TOE ECULE	E CHA NGTH: PE: & RANDE POLOG E TYI n: Ba	RACT 480 imino EDNES SY: ] PE: [	TERIS  aci  aci  Ss: s  lines  prote  lus s	STICS ino a id sing! ar ein amylo	S: acids le oliq	uefac		3					
35	. (	(i) (ii) (iii) (xi)	SEQU (A) (B) (C) (D) MOLE	JENCE TYPE STI TOPE ECULI ANIST JENCE	E CHA IGTH: PE: E RANDE POLOG E TYI M: BE E DES	RACT HARDNES SY: I PE: I ACILI	TERIS  acid  SS: solines  prote  tus solus  TION	STICS ino a id sing! sin sin amylo N: SE	S: acids le oliqu EQ II	lefac	5:		Tyr	Thr	Pro	Asn 15	Asp
The with math hard of the state	(	(i) (ii) (iii) (xi) Val	SEQU (A) (B) (C) (D) MOLE Orga	JENCE LEN TYE STE TOE ECULE Anist DENCE	E CHZ IGTH: PE: E RANDE POLOG E TYPE IN: BE E DES	ARACT 480 amino EDNES EY: I PE: I SCRIE Leu 5	TERIS  D ami D aci SS: S  Lines Drote Lus a  PTION  Met	STICS ino a id sing ar ein amylo N: SE	S: acids le oliqu EQ II	lefac NO: Phe	5: Glu 10	Trp				15	_
35	(	(i) (ii) (iii) (xi) Val 1 Gly	SEQU (A) (B) (C) (D) MOLE Orga SEQU Asn	JENCE LEN TYPE STE TOPECULE ANIST DENCE Gly His	E CHZ IGTH: PE: a RANDE POLOG E TYP IN: Ba E DES Thr Trp 20	ARACT 480 AMINO EDNES SY: 1 PE: P ACILL SCRIE Leu 5	TERIS  Description  SS: selines  protection  Met  Arg	ino a id ing ing in	S: acids le Oliqu EQ II Tyr	nefac ) NO: Phe Asn 25	5: Glu 10 Asp	Trp Ala	Glu	His	Leu 30	15 Ser	Asp
The with math hard of the state	(	(i) (ii) (iii) (xi) Val 1 Gly Ile	SEQU (A) (B) (C) (D) MOLE Orga SEQU Asn	JENCE LEN TYE STE TOE ECULE ANIST JENCE Gly His Ile 35	E CHZ IGTH: PE: 2 PE: 2 PE: 2 POLOG POLOG TYP  Trp  Trp  Thr	ARACT : 480 camino EDNES SY: ] PE: ] acill GCRIF Leu 5 Lys Ala	TERIS  TE	STICS ino a id single sin amylo 7: SF Gln Leu	S: Acids le clique Tyr Gln Ile 40	Phe Asn 25	5: Glu 10 Asp Pro	Trp Ala Ala	Glu Tyr	His Lys 45	Leu 30 Gly	15 Ser Leu	Asp Ser
The section metric from the section metric section from the section from t	. ((	(ii) (iii) (iii) (xi) Val 1 Gly Ile Gln	SEQUENCE (A) (B) (C) (D) (MOLE Organis SEQUENCE (C) (A) (C) (C) (C) (C) (C) (C) (C) (C) (C) (C	JENCE LEN TYPE STE TOOL ECULE ANIST JENCE Gly His Ile 35	E CHZ IGTH: PE: E RANDE POLOG E TYP Thr Trp 20 Thr Asn	ARACT 480 amino EDNES EV: 1 PE: 1 Accill 6CRIE Leu 5 Lys Ala Gly	TERIS  AME  SELITOR  MET  Arg  Val	STICS ino s id ino s in ir in amylo I: SI Gln Leu Trp Gly 55	S: acids le clique EQ II Tyr Gln Ile 40 Pro	Phe Asn 25 Pro	5: Glu 10 Asp Pro	Trp Ala Ala Leu	Glu Tyr Tyr 60	His Lys 45 Asp	Leu 30 Gly Leu	15 Ser Leu Gly	Asp Ser Glu
The section metric from the section metric section from the section from t		(ii) (iii) (xi) (xi) Val 1 Gly Ile Gln Phe 65	SEQUENCE (A) (B) (C) (C) (MOLE OF GEO C) (C) (C) (C) (C) (C) (C) (C) (C) (C)	JENCE LEN TYE STE TOLE ANDENCE Gly His Ile 35 Amp	E CHZ IGTH: PE: E PE: E PANDE POLOGE TYP  TO THY  Asn  Lys	ARACTIC 480 amino STATE 1925 I PE : I	TERIS  AME  SS: E  Lines  Line	STICS ino a id single sin amylo N: SE Gln Leu Trp Gly SS Val	S: acids le clique EQ II Tyr Gln Ile 40 Pro	Phe Asn 25 Pro Tyr	5: Glu 10 Asp Pro Asp	Trp Ala Ala Leu Tyr	Glu Tyr Tyr 60 Gly	His Lys 45 Asp	Leu 30 Gly Leu Lys	15 Ser Leu Gly Ser	Asp Ser Glu Glu 80
35 0 0 45 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	. ((	(ii) (iii) (iii) (xi) Val 1 Gly Ile Gln Phe 65	SEQUENCE (A) (B) (C) (C) (D) (C) (C) (C) (C) (C) (C) (C) (C) (C) (C	JENCE LEN TYPE STEE TOOLECULE AND STEE COULT AND ST	E CHZ IGTH: PE: 2 PE: 2 PE: 2 PE: 3 PE: 3 PE: 4 POLOG	ARACTE 480 amino ESTATE IN THE PERSON IN THE	TERISO AMEDICAL SERVICES: SERVICES FOR SERVI	STICS ino s id single in amylo S: SI Gln Leu Trp Gly 55 Val Ser	S: acids le clique EQ II Tyr Gln Ile 40 Pro Arg	Phe Asn 25 Pro Tyr Thr	5: Glu 10 Asp Pro Asp Lys Ser 90	Trp Ala Ala Leu Tyr 75 Arg	Glu Tyr Tyr 60 Gly Asn	His Lys 45 Asp Thr	Leu 30 Gly Leu Lys Gln	15 Ser Leu Gly Ser Val 95	Asp Ser Glu Glu 80

		Glu	Glu 130	Tyr	Gln	Ile	Lys	Ala 135	Trp	Thr	qsA	Phe	Arg 140		Pro	Gly	Arg
	5	Gly 145	Asn	Thr	Tyr	Ser	Asp 150	Phe	Lys	Trp	His	Trp 155	Tyr	Hıs	Phe	Ąsp	Gly 160
		Ala	Asp	Trp	Asp	Glu 165	Ser	Arg	Lys	Ile	Ser 170	Arg	Ile	Phe	Lys	Phe 175	Arg
	10	Gly	Glu	Gly	Lys 180	Ala	Trp	Asp	Trp	Glu 185		Ser	Ser	Glu	Asn 190	Gly	Asn
	15	Tyr	Asp	Tyr 195	Leu	Met	Tyr	Ala	Авр 200	Val	Asp	Tyr	Asp	His 205	Pro	Asp	Val
		Val	Ala 210	Glu	Thr	Lys	Lys	Trp 215	Gly	Ile	Trp	Tyr	Ala 220	Asn	Glu	Leu	Ser
	20	Leu 225	Asp	Gly	Phe	Arg	Ile 230	Asp	Ala	Ala	Lys	Hie 235	Ile	Lys	Phe	Ser	Phe 240
the Hall	1	Leu	Arg	Asp	Trp	Val 245	Gln	Ala	Val	Arg	Gln 250	Ala	Thr	Gly	Lys	Glu 255	Met
Halla Balla B	= 23 = = =	Phe	Thr	Val	Ala 260	Glu	Tyr	Trp	Gln	Asn 265	Asn	Ala	Gly	Lys	Leu 270	Glu	Asn
11.	<u></u> 30	Tyr	Leu	Asn 275	Lys	Thr	Ser	Phe	Asn 280	Gln	Ser	Val	Phe	Asp 285	Val	Pro	Leu
Here and		His	Phe 290	Asn	Leu	Gln	Ala	Ala 295	Ser	Ser	Gln	Gly	Gly 300	Gly	Tyr	Asp	Met
H ndh salh	_35 _	Arg 305	Arg	Leu	Leu	Asp	Gly 310	Thr	Val	Val	Ser	Arg 315	His	Pro	Glu	Lys	Ala 320
101		Val	Thr	Phe	Val	Glu 325	Aøn	His	Asp	Thr	Gln 330	Pro	Gly	Gln	Ser	Leu 335	Glu
1	or of the state of	Ser	Thr	Val	Gln 340	Thr	Trp	Phe	Lys	Pro 345	Leu	Ala	Tyr	Ala	Phe 350	Ile	Leu
	45	Thr	Arg	Glu 355	Ser	Gly	Tyr	Pro	Gln 360	Val	Phe	Tyr	Gly	Asp 365	Met	Tyr	Gly
		Thr	<b>L</b> ув 370	Gly	Thr	Ser	Pro	Lys 375	Glu	Ile	Pro	Ser	Leu 380	Lys	Asp	Asn	Ile
	50	Glu 385	Pro	Ile	Leu	Lys	Ala 390	Arg	Lys	Glu	Tyr	Ala 395	Tyr	Gly	Pro	Gln	His 400
		Asp	Тут	Ile	Asp	His 405	Pro	Asp	Val	Ile	Gly 410	Trp	Thr	Arg	Glu	Gly 415	Asp
	55	Ser	Ser	Ala	Ala 420	Lys	Ser	Gly	Leu	Ala 425	Ala	Leu	Ile	Thr	Asp 430	Gly	Pro
	60	Gly	Gly	<b>Ser</b> 435	Lys	Arg	Met	Tyr	Ala 440	Gly	Leu	Lys	Asn	Ala 445	Gly	Glu	Thr
		Trp	Tyr 450	Asp	Ile	Thr	Gly	Asn 455	Arg	Ser	Aap	Thr	Val 460	Lys	Ile	Gly	Ser
	65	Asp 465	Gly	Trp	Gly	Glu	Phe 470	His	Val	Asn	Asp	Gly 475	Ser	Val	Ser	Ile	Tyr 490

5	(2)	4	SEC (A (B (C	UENC L) LE L) TY L) ST L) TO	E CH NGTH PE: RAND	IARAC I: 48 amin EDNE GY:	ID N CTERI S5 am so ac SSS: line prot	STIC ino id sing ar	S: acid	ls							
10		(iii	)Org	anis	m: P	Bacil	lus PTIO	sp.	EQ I	D NO	: 6:						
15		His 1	His	Asn	Gly	Thr 5	Asn	Gly	Thr	Met	Met 10	Gln	Туг	Phe	Glu	Trp 15	Туз
		Leu	Pro	Asn	Авр 20	Gly	Asn	His	Trp	Asn 25	Arg	Leu	Aen	Ser	Asp 30	Ala	Set
20		Asn	Leu	Lys 35	Ser	Lys	Gly	Ile	Thr 40	Ala	Val	Trp	Ile	Pro 45	Pro	Ala	Tr
25		Lys	Gly 50	Ala	Ser	Gln	Asn	Asp 55	Val	Gly	Tyr	Gly	Ala 60	Tyr	Ąap	Leu	ТУ1
		Asp 65	Leu	Gly	Glu	Phe	Asn 70	Gln	Lys	Gly	Thr	Val 75	Arg	Thr	Lys	Tyr	Gl <sub>3</sub> 80
30		Thr	Arg	Ser	Gln	Leu 85	Gln	Ala	Ala	Val	Thr 90	Ser	Leu	Lys	Asn	Asn 95	Gly
		lle	Gln	Val	Tyr 100	Gly	Asp	Val	Val	Met 105	Asn	His	Lys	Gly	Gly 110	Ala	Asp
35		Ala	Thr	Glu 115	Met	Val	Arg	Ala	Val 120	Glu	Val	Asn	Pro	Asn 125	Asn	Arg	Asn
40		Gln	Glu 130	Val	Thr	Gly	Glu	Tyr 135	Thr	Ile	Glu	Ala	Trp 140	Thr	Arg	Phe	Asp
		Phe 145	Pro	Gly	Arg	Gly	Asn 150	Thr	His	Ser	Ser	Phe 155	Lys	Trp	Arg	Trp	Tyr 160
45		His	Phe	Asp	Gly	Val 165	Asp	Trp	Asp	Gln	Ser 170	Arg	Arg	Leu	Asn	Asn 175	Arg
		Ile	Tyr	Lys	Phe 180	Arg	Gly	His	Gly	Lys 185	Ala	Trp	Asp	Trp	Glu 190	Val	Asp
50		Thr	Glu	Asn 195	Gly	Asn	Tyr	Asp	Tyr 200	Leu	Met	Tyr	Ala	Asp 205	Ile	Asp	Met
55		Asp	His 210	Pro	Glu	Val	Val	Asn 215	Glu	Leu	Arg	Asn	Trp 220	Gly	Val	Trp	Tyr
		Thr 225	Asn	Thr	Leu	Gly	Leu 230	Asp	Gly	Phe	Arg	Ile 235	Asp	Ala	Val	Lys	His 240
60		Ile	Lys	Tyr	Ser	Phe 245	Thr	Arg	Asp	Trp	Ile 250	Asn	His	Val	Arg	Ser 255	Ala
		Thr	Gly	Lys	Asn 260	Met	Phe	Ala	Val	Ala 265	Glu	Phe	Trp	Lys	Asn 270	Asp	Leu
65		Gly	Ala	Ile 275	Glu	Asn	Туг	Leu	Gln 280	Lys	Thr	Asn	Trp	Asn 285	His	Ser	Val

		Phe	Asp 290	Val	Pro	Leu	His	Туг 295	Asn	Leu	Tyr	Asn	Ala 300	Ser	ГУs	Ser	Gly
5		Gly 305	Авп	Tyr	Asp	Met	Arg 310	Asn	Ile	Phe	Asn	Gly 315	Thr	Val	Val	Gln	Arg 320
		His	Pro	Ser	His	Ala 325	Val	Thr	Phe	Val	<b>Авр</b> 330	Asn	His	Asp	Ser	Gln 335	Pro
10		Glu	Glu	Ala	Leu 340	Glu	Ser	Phe	Val	Glu 345	Glu	Trp	Phe	Lys	Pro 350	Leu	Ala
15		Tyr	Ala	Leu 355	Thr	Leu	Thr	Arg	Glu 360	Gln	Gly	Tyr	Pro	Ser 365	Val	Phe	Tyr
		Gly	Авр 370	Tyr	Tyr	Gly	Ile	Pro 375	Thr	His	Gly	Val	Pro 380	Ala	Met	Arg	ser
20		Lys 385	Ile	Asp	Pro	Ile	Leu 390	Glu	Ala	Arg	Gln	Lys 395	Tyr	Ala	Tyr	Gly	Lys 400
		Gln	Asn	Asp	Tyr	Leu 405	Asp	His	His	Asn	Ile 410	Ile	Gly	Trp	Thr	Arg 415	Glu
25		Gly	Asn	Thr	Ala 420	His	Pro	Asn	Ser	Gly 425	Leu	Ala	Thr	Ile	Met 430	Ser	Asp
30		Gly	Ala	Gly 435	Gly	Ser	Lys	Trp	Met 440	Phe	Val	Gly	Arg	Asn 445	Lys	Ala	Gly
		Gln	Val 450	Trp	Ser	Asp	Ile	Thr 455	Gly	Asn	Arg	Thr	Gly 460	Thr	Val	Thr	Ile
35		A61 465	Ala	Asp	Gly	Trp	Gly 470	Asn	Phe	Ser	Val	Asn 475	Gly	Gly	Ser	Val	Ser 490
		Ile	TTP	Val	Asn	Lys 485											
40	(2)	INFOI (i)	SEQ( (A) (B)	JENCI LEN TYI	CHI IGTH: PE: 8	ARACT 485	reris 5 ami 5 aci	TICS ino a id	S: acids	5							
45		(ii) (iii) (xi)	(D) MOLI Orga	TOP CULI Inism	POLOC E TYI n: Ba	SY: ] PE: p acil.	linea prote lus s	ein sp.		O NO:	: 7:						
50		His 1	His	Asn	Gly	Thr 5	Asn	Gly	Thr	Met	Met 10	Gln	Tyr	Phe	Glu	Trp 15	Tyr
55		Leu	Pro	Asn	Asp 20	Gly	Asn	His	Trp	Asn 25	Arg	Leu	Arg	Asp	Asp 30	Ala	Ala
33		Asn	Leu	Lys 35	Ser	Lys	Gly	Ile	Thr 40	Ala	Val	Trp	Ile	Pro 45	Pro	Ala	Trp
60		ГЛЗ	617 20	Thr	Ser	Gln	Asn	Asp 55	Val	Gly	Tyr	Gly	Ala 60	Tyr	Asp	Leu	Tyr
		Asp 65	Leu	Gly	Glu	Phe	Asn 70	Gln	Lys	Gly	Thr	Val 75	Arg	Thr	Lys	Tyr	Gly 80
65		Thr	Arg	Asn	Gln	Leu 85	Gln	Ala	Ala	Val	Thr 90	Ser	Leu	Lys	Asn	Asn 95	Gly

15	
S	la Asp
130 135 140 150 140 150 160 161 161 160 161 165 160 165 165 165 165 165 165 165 165 165 165	rg Asn
His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln A 165  The Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Gly Val Pro 195  Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Pro 205  Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Pro 225  Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val I 225  Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp 266  Gly Ala Ile Glu Asn Tyr Leu Asn Leu Tyr Asn Ala Ser Asn S 266  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn S 295  Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 340  His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro 365  Gly Ala Leu Val Leu Thr Arg Gln Gln Tyr Pro 365  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  So Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Asp His His Asp Ile Ile Gly Trp Thr And Ala Ser Asp Ile Leu Asp Ile Ile Gly Trp Thr And Ala Ser Asp Ile Leu Ala Arg Gln Thr Phe Ala Tyr Gly Asp Asp His His Asp Ile Ile Gly Trp Thr And Ile Gly Asp Ser Ser His Pro Asp His His Asp Ile Ile Gly Trp Thr And Ile Gly Asp Ser Ser His Pro Asp Ser Gly Leu Ala Thr Ile Met Sep Ile Asp Ser Ser His Pro Asp Ser Gly Leu Ala Thr Ile Met Sep Ile Gly Asp Ser Ser His Pro Asp Ser Gly Leu Ala Thr Ile Met Sep Ile Ala Thr Ile Ala Thr Ile Met Sep Ile Ala Thr Ile Ala Thr Ile Met Sep Ile Ala Thr	he Asp
165	rp Tyr 160
The Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu V 180  Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val F 200  Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val T 220  Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val I 225  Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val I 225  The Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Ala 270  Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn His S 270  Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His S 285  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn S 295  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn S 295  Gly Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gly Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 325  Gly Ala Leu Val Leu Thr Arg Glu Gln Gln Trp Phe Lys Pro I 360  Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val F 370  Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val F 370  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 375  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Cly	sn Lys 75
20	al Asp
210 215 220  25 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val I 225  1le Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asp 245  Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp 270  Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser 275  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser 295  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser 295  His Pro Thr His Ala Val Thr Phe Val Asn Asn His Asp Ser Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 325  Gly Glu Ala Leu Glu Ser Phe Val Gln Gly Tyr Pro Ser Val Fer 325  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  Gly Asp Tyr Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Ser Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Ser Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Ser Gly Asn Thr Ile Met Ser Asn Ser Gly Asn Thr Ile Met Ser Asn Ser Gly Asn Thr Ile Met Ser Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Ser Gly Asn Thr Ile Met Ser Asn Ser Gly Leu Ala Thr Ile Met Ser	sp Met
225 230 235  Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg A 250  Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn A 265  Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His 285  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn S 295  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn S 300  Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gly Ser Val Val Gly Gly Glu Ala Leu Glu Ser Phe Val Asp Asn His Asp Ser G 335  Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 345  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	rp Tyr
Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn A 265  Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His S 285  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn S 295  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn S 300  Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val G 305  His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser G 330  Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 350  Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val F 365  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr G 385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	ys His 240
Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn A 260  Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser 285  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser 290  40 Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gen 305  His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gen Asn Ser 325  Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro In 345  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met In 370  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met In 385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr And And And And And In Ile Met Ser Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Ser His Pro Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Ser His Pro Asn Ser Ser Gly Leu Ala Thr Ile Met Ser Ser His Pro Asn Ser Gly Pro Asn Ser G	sn Thr
275  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser 295  40 Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gly 305  His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 345  Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 350  Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val F 365  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  Styr Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly 385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser	sp Leu
290 295 300 40 Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gly Sor Val Val Gly Sor Val Val Gly Sor Val Val Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 345 Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 350 Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val F 365 Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  55 Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly 385 Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405 Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser	er Val
His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser G 325  Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 340  Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val F 355  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr G 385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	er Gly
Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 340  Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val F 365  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr G 385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	ln Lys 320
Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro I 340  Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val F 365  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr G 385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	ln Pro 35
Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met I 370  Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr G 385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	eu Ala
370  375  380  Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr G 385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	he Tyr
385  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr A 405  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	ys Ser
405 410 4  60  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	ly Thr 400
Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met S	rg Glu 15
	er Asp
Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys A	la Gly
Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val T	hr Ile

450 455 Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser Val Trp Val Lys Gln (2) INFORMATION FOR SEQ ID NO: 8: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 485 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (iii) Organism: Bacillus sp. 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His 20 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser 25 Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Э0 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly 65 70 75 80 Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly 85 90 95 35 Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp 105 Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn 40 Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp 130 135 140 45 Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg 50 170 Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp 55 Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met 200 Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr €0 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala 65 Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu

				260					265					270			
	Gly	Ala	Leu 275	Glu	Asn	Tyr	Leu	Asn 280	Lys	Thr	Asn	Trp	Asn 285	His	Ser	Val	
5	Phe	Asp 290	Val	Pro	Leu	His	Tyr 295	Asn	Leu	Tyr	Asn	Ala 300	Ser	Asn	Ser	Gly	
10	Gly 305	Asn	Tyr	Asp	Met	Ala 310	ГÀг	Leu	Leu	Asn	Gly 315	Thr	Val	Val	Gln	Lys 320	
	His	Pro	Met	His	Ala 325	Val	Thr	Phe	Val	Авр 330	Asn	His	Asp	Ser	Gln 335	Pro	
15	Gly	Glu	Ser	Leu 340	Glu	Ser	Phe	Val	Gln 345	Glu	Trp	Phe	Lys	Pro 350	Leu	Ala	
20	Tyr	Ala	Leu 355	Ile	Leu	Thr	Arg	Glu 360	Gln	Gly	Tyr	Pro	Ser 365	Val	Phe	Tyr	
20	Gly	<b>Asp</b> 370		Tyr	Gly	Ile	Pro 375	Thr	His	Ser	Val	Pro 380	Ala	Met	Ly\$	Ala	
25	Lys 385	Ile	Asp	Pro	Ile	Leu 390	Glu	Ala	Arg	Gln	Asn 395	Phe	Ala	Tyr	Gly	Thr 400	
	Gln	His	Asp	Tyr	Phe 405	Asp	His	His	Asn	11e 410	Ile	Gly	Trp	Thr	Arg 415	Glu	
30	Gly	Asn	Thr	Thr 420	His	Pro	Asn	Ser	Gly 425	Leu	Ala	Thr	Ile	Met 430	Ser	Asp	
35	Gly	Pro	Gly 435	Gly	Glu	Lys	Trp	Met 440	Tyr	Val	Gly	Gln	Asn 445	ГЛа	Ala	Gly	
	Gln	Val 450	Trp	His	Asp	Ile	Thr 455	Gly	Asn	Lys	Pro	Gly 460	Thr	Val	Thr	Ile	
40	Asn 465	Ala	Asp	Gly	Trp	Ala 470	Asn	Phe	Ser	Val	Asn 475	Gly	Gly	Ser	Val	Ser 480	
	Ile	Trp	Val	Lys	Arg 485												
45	(2) INFOI (i)	SEQ(A)	JENCI LEI	E CHU NGTH	ARACT	TERIS	STICS		<b>3</b>								
50	(ii) (iii ( <b>x</b> i)	(C) (D) MOL) Org:	anis	RANDI POLOG E TYI m: Ba	EDNES SY: PE: I acil	SS: & linea DNA lus &	sing ar (geno sp.	omic)		: 9:							
55	CATCATAA	IG G	AACA	AATGO	G TAC	TATO	SATG	CAA	CATT	rcg /	<b>A</b> ATG(	STAT?	PT GO	CAA	ATGA	2	60
	GGGAATCA	TT G	GAAC	AGGT	r gag	GGA:	rgac	GCA	GCTA!	ACT :	)AAA1	SAGT	AA AA	GGA.	raaca	£.	120
60	GCTGTATG	GA T	CCCA	CIG	CATO	GAA	GGG	ACT	rcccz	AGA A	ATGA:	rgtad	GG T	TATG	SAGC	3	180
	TATGATTT	AT A	rga <b>r</b> (	CTTG	G AG	AGTT	raac	CAG	AAGG(	GGA (	CGGT	rcgtz	AC AZ	TAAL	\TGG!	4	240
	ACACGCAA	CC A	GCTA(	CAGG	C TG	CGGT	GACC	TCT	LAATI	AAA	AATA	CGGC	AT TO	CAGG'	ATA1	r	300
65	GGTGATGT	CG T	CATG	AATC	A TA	AAGG:	rgga	GCA	BATG	ETA (	CGGAI	ATTO	T A	AATG	CGGT	Ą	360
	GAAGTGAA	דר פו	SAGC	אככנ	2 44 2	CCAC	מ מ ב	ACC-	רכאכנ	מ מב	מתמ	TGCA	ነ አ	ממבב	CTG	2	420

14

	ACAAAGTTTG ATTTTCCTGG AAGAGGAAAT AACCATTCCA GCTTTAAGTG GCGCTGGTAT	480
_	CATTTTGATG GGACAGATTG GGATCAGTCA CGCCAGCTTC AAAACAAAAT ATATAAATTC	540
5	AGGGGAACAG GCAAGGCCTG GGACTGGGAA GTCGATACAG AGAATGGCAA CTATGACTAT	600
	CTTATGTATG CAGACGTGGA TATGGATCAC CCAGAAGTAA TACATGAACT TAGAAACTGG	660
10	GGAGTGTGGT ATACGAATAC ACTGAACCTT GATGGATTTA GAATAGATGC AGTGAAACAT	720
	ATAAAATATA GCTTTACGAG AGATTGGCTT ACACATGTGC GTAACACCAC AGGTAAACCA	780
	ATGTTTGCAG TGGCTGAGTT TTGGAAAAAT GACCTTGGTG CAATTGAAAA CTATTTGAAT	840
15	AAAACAAGTT GGAATCACTC GGTGTTTGAT GTTCCTCTCC ACTATAATTT GTACAATGCA	900
	TCTAATAGCG GTGGTTATTA TGATATGAGA AATATTTTAA ATGGTTCTGT GGTGCAAAAA	960
20	CATCCAACAC ATGCCGTTAC TTTTGTTGAT AACCATGATT CTCAGCCCGG GGAAGCATTG	1020
	GAATCCTTTG TTCAACAATG GTTTAAACCA CTTGCATATG CATTGGTTCT GACAAGGGAA	1080
	CAAGGTTATC CTTCCGTATT TTATGGGGAT TACTACGGTA TCCCAACCCA TGGTGTTCCG	1140
25	GCTATGAAAT CTAAAATAGA CCCTCTTCTG CAGGCACGTC AAACTTTTGC CTATGGTACG	1200
	CAGCATGATT ACTITGATCA TCATGATATT ATCGGTTGGA CAAGAGAGGG AAATAGCTCC	1260
30	CATCCAAATT CAGGCCTTGC CACCATTATG TCAGATGGTC CAGGTGGTAA CAAATGGATG	1320
	TATGTGGGGA AAAATAAAGC GGGACAAGTT TGGAGAGATA TTACCGGAAA TAGGACAGGC	1380
7.6	ACCGTCACAA TTAATGCAGA CGGATGGGGT AATTTCTCTG TTAATGGAGG GTCCGTTTCG	1440
35	GTTTGGGTGA AGCAA	1455
40	(2) INFORMATION FOR SEQ ID NO: 10:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 1455 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic) (iii)Organism: Bacillus sp. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
	CATCATAATG GGACAAATGG GACGATGATG CAATACTTTG AATGGCACTT GCCTAATGAT	€0
50	GGGAATCACT GGAATAGATT AAGAGATGAT GCTAGTAATC TAAGAAATAG AGGTATAACC	120
	GCTATTTGGA TTCCGCCTGC CTGGAAAGGG ACTTCGCAAA ATGATGTGGG GTATGGAGCC	180
55	TATGATCTTT ATGATTTAGG GGAATTTAAT CAAAAGGGGA CGGTTCGTAC TAAGTATGGG	240
23	ACACGTAGTC AATTGGAGTC TGCCATCCAT GCTTTAAAGA ATAATGGCGT TCAAGTTTAT	300
	GGGGATGTAG TGATGAACCA TAAAGGAGGA GCTGATGCTA CAGAAAACGT TCTTGCTGTC	360
60	GAGGTGAATC CAAATAACCG GAATCAAGAA ATATCTGGGG ACTACACAAT TGAGGCTTGG	420
	ACTAAGTTTG ATTTTCCAGG GAGGGGTAAT ACATACTCAG ACTTTAAATG GCGTTGGTAT	480
65	CATTTCGATG GTGTAGATTG GGATCAATCA CGACAATTCC AAAATCGTAT CTACAAATTC	540
05	CONCENTRATE CTANGERATE CONTROLENA CTACATTECE ANAMOGANA TENTENTENT	600

CGAGGTGATG GTAAGGCATG GGATTGGGAA GTAGATTCGG AAAATGGAAA TTATGATTAT



15

	TTAATGTATG CAGATGTAGA TATGGATCAT CCGGAGGTAG TAAATGAGCT TAGAAGATGG	660
	GGAGAATGGT ATACAAATAC ATTAAATCTT GATGGATTTA GGATCGATGC GGTGAAGCAT	720
5	ATTAAATATA GCTTTACACG TGATTGGTTG ACCCATGTAA GAAACGCAAC GGGAAAAGAA	780
	ATGTTTGCTG TTGCTGAATT TTGGAAAAAT GATTTAGGTG CCTTGGAGAA CTATTTAAAT	840
10	AAAACAAACT GGAATCATTC TGTCTTTGAT GTCCCCCTTC ATTATAATCT TTATAACGCG	900
10	TCAAATAGTG GAGGCAACTA TGACATGGCA AAACTTCTTA ATGGAACGGT TGTTCAAAAG	960
	CATCCAATGC ATGCCGTAAC TTTTGTGGAT AATCACGATT CTCAACCTGG GGAATCATTA	1020
15	GAATCATTTG TACAAGAATG GTTTAAGCCA CTTGCTTATG CGCTTATTTT AACAAGAGAA	1080
	CAAGGCTATC CCTCTGTCTT CTATGGTGAC TACTATGGAA TTCCAACACA TAGTGTCCCA	1140
20	GCAATGAAAG CCAAGATTGA TCCAATCTTA GAGGCGCGTC AAAATTTTGC ATATGGAACA	1200
	CAACATGATT ATTTTGACCA TCATAATATA ATCGGATGGA CACGTGAAGG AAATACCACG	1260
	CATCCCAATT CAGGACTTGC GACTATCATG TCGGATGGGC CAGGGGGAGA GAAATGGATG	1320
25	TACGTAGGGC AAAATAAAGC AGGTCAAGTT TGGCATGACA TAACTGGAAA TAAACCAGGA	1380
	ACAGTTACGA TCAATGCAGA TGGATGGGCT AATTTTTCAG TAAATGGAGG ATCTGTTTCC	1440
30	ATTTGGGTGA AACGA	1455
35 40	(2) INFORMATION FOR SEQ ID NO: 11:     (i) SEQUENCE CHARACTERISTICS:         (A) LENGTH: 1548 base pairs         (B) TYPE: nucleic acid         (C) STRANDEDNESS: single         (D) TOPOLOGY: linear     (ii) MOLECULE TYPE: DNA (genomic)     (iii) Organism: Bacillus stearothermophilus     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
	GCCGCACCGT TTAACGGCAC CATGATGCAG TATTTTGAAT GGTACTTGCC GGATGATGGC	60
4 =	ACGTTATGGA CCAAAGTGGC CAATGAAGCC AACAACTTAT CCAGCCTTGG CATCACCGCT	120
45	CTTTGGCTGC CGCCCGCTTA CAAAGGAACA AGCCGCAGCG ACGTAGGGTA CGGAGTATAC	180
	GACTTGTATG ACCTCGGCGA ATTCAATCAA AAAGGGACCG TCCGCACAAA ATACGGAACA	240
50	AAAGCTCAAT ATCTTCAAGC CATTCAAGCC GCCCACGCCG CTGGAATGCA AGTGTACGCC	300
	GATGTCGTGT TCGACCATAA AGGCGGCGCT GACGGCACGG AATGGGTGGA CGCCGTCGAA	360
55	GTCAATCCGT CCGACCGCAA CCAAGAAATC TCGGGCACCT ATCAAATCCA AGCATGGACG	420
	AAATTTGATT TTCCCGGGCG GGGCAACACC TACTCCAGCT TTAAGTGGCG CTGGTACCAT	480
	TTTGACGGCG TTGATTGGGA CGAAAGCCGA AAATTGAGCC GCATTTACAA ATTCCGCGGC	540
60	ATCGGCAAAG CGTGGGATTG GGAAGTAGAC ACGGAAAACG GAAACTATGA CTACTTAATG	600
	TATGCCGACC TTGATATGGA TCATCCCGAA GTCGTGACCG AGCTGAAAAA CTGGGGGAAA	660
	TGGTATGTCA ACACAACGAA CATTGATGGG TTCCGGCTTG ATGCCGTCAA GCATATTAAG	720

TICAGTTTTT TTCCTGATTG GTTGTCGTAT GTGCGTTCTC AGACTGGCAA GCCGCTATTT

16

	ACCGTCGGGG AATATTGGAG CTATGACATC AACAAGTTGC ACAATTACAT TACGAAAACA	840
	GACGGAACGA TGTCTTTGTT TGATGCCCCG TTACACAACA AATTTTATAC CGCTTCCAAA	900
5	TCAGGGGGCG CATTTGATAT GCGCACGTTA ATGACCAATA CTCTCATGAA AGATCAACCG	960
	ACATTGGCCG TCACCTTCGT TGATAATCAT GACACCGAAC CCGGCCAAGC GCTGCAGTCA	1020
10	TGGGTCGACC CATGGTTCAA ACCGTTGGCT TACGCCTTTA TTCTAACTCG GCAGGAAGGA	1080
10	TACCCGTGCG TCTTTTATGG TGACTATTAT GGCATTCCAC AATATAACAT TCCTTCGCTG	1140
	AAAAGCAAAA TCGATCCGCT CCTCATCGCG CGCAGGGATT ATGCTTACGG AACGCAACAT	1200
15	GATTATCTTG ATCACTCCGA CATCATCGGG TGGACAAGGG AAGGGGGGCAC TGAAAAACCA	1260
	GGATCCGGAC TGGCCGCACT GATCACCGAT GGGCCGGGAG GAAGCAAATG GATGTACGTT	1320
20	GGCAAACAAC ACGCTGGAAA AGTGTTCTAT GACCTTACCG GCAACCGGAG TGACACCGTC	1380
20	ACCATCAACA GTGATGGATG GGGGGAATTC AAAGTCAATG GCGGTTCGGT TTCGGTTTGG	1440
	GTTCCTAGAA AAACGACCGT TTCTACCATC GCTCGGCCGA TCACAACCCG ACCGTGGACT	1500
25	GGTGAATTCG TCCGTTGGAC CGAACCACGG TTGGTGGCAT GGCCTTGA	1548
35	(i) SEQUENCE CHARACTERISTICS:         (A) LENGTH: 1920 base pairs         (B) TYPE: nucleic acid         (C) STRANDEDNESS: single         (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic) (iii) Organism: Bacillus licheniformis (ix) FEATURE:         (A) NAME/KEY: CDS         (B) LOCATION: 421. 1872  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
	CGGAAGATTG GAAGTACAAA AATAAGCAAA AGATTGTCAA TCATGTCATG	60
	GAGACGGAAA AATCGTCTTA ATGCACGATA TTTATGCAAC GTTCGCAGAT GCTGCTGAAG	120
45	AGATTATTAA AAAGCTGAAA GCAAAAGGCT ATCAATTGGT AACTGTATCT CAGCTTGAAG	180
	AAGTGAAGAA GCAGAGAGGC TATTGAATAA ATGAGTAGAA GCGCCATATC GGCGCTTTTC	240
50	TTTTGGAAGA AAATATAGGG AAAATGGTAC TTGTTAAAAA TTCGGAATAT TTATACAACA	300
J 0	TCATATGTTT CACATTGAAA GGGGAGGAGA ATCATGAAAC AACAAAAACG GCTTTACGCC	360
	CGATTGCTGA CGCTGTTATT TGCGCTCATC TTCTTGCTGC CTCATTCTGC AGCAGCGGCG	420
55	GCA AAT CTT AAT GGG ACG CTG ATG CAG TAT TTT GAA TGG TAC ATG CCC	468
	AAT GAC GGC CAA CAT TGG AGG CGT TTG CAA AAC GAC TCG GCA TAT TTG	516
60	GCT GAA CAC GGT ATT ACT GCC GTC TGG ATT CCC CCG GCA TAT AAG GGA	564
30	ACG AGC CAA GCG GAT GTG GGC TAC GGT GCT TAC GAC CTT TAT GAT TTA	612
	GGG GAG TTT CAT CAA AAA GGG ACG GTT CGG ACA AAG TAC GGC ACA AAA	660
65	GGA GAG CTG CAA TCT GCG ATC AAA AGT CTT CAT TCC CGC GAC ATT AAC	708

GTT TAC GGG GAT GTG GTC ATC AAC CAC AAA GGC GGC GCT GAT GCG ACC

60

17

GAA GAT GTA ACC GCG GTT GAA GTC GAT CCC GCT GAC CGC AAC CGC GTA 804 ATT TCA GGA GAA CAC CTA ATT AAA GCC TGG ACA CAT TTT CAT TTT CCG 852 GGG CGC GGC AGC ACA TAC AGC GAT TTT AAA TGG CAT TGG TAC CAT TTT 900 GAC GGA ACC GAT TGG GAC GAG TCC CGA AAG CTG AAC CGC ATC TAT AAG 948 10 TTT CAA GGA AAG GCT TGG GAT TGG GAA GTT TCC AAT GAA AAC GGC AAC 996 TAT GAT TAT TTG ATG TAT GCC GAC ATC GAT TAT GAC CAT CCT GAT GTC 1044 GCA GCA GAA ATT AAG AGA TGG GGC ACT TGG TAT GCC AAT GAA CTG CAA 1092 15 TTG GAC GGT TTC CGT CTT GAT GCT GTC AAA CAC ATT AAA TTT TCT TTT 1140 TTG CGG GAT TGG GTT AAT CAT GTC AGG GAA AAA ACG GGG AAG GAA ATG 1188 20 TTT ACG GTA GCT GAA TAT TGG CAG AAT GAC TTG GGC GCG CTG GAA AAC 1236 TAT TTG AAC AAA ACA AAT TTT AAT CAT TCA GTG TTT GAC GTG CCG CTT 1284 CAT TAT CAG TTC CAT GCT GCA TCG ACA CAG GGA GGC GGC TAT GAT ATG 1332 AGG AAA TTG CTG AAC GGT ACG GTC GTT TCC AAG CAT CCG TTG AAA TCG 1380 GTT ACA TTT GTC GAT AAC CAT GAT ACA CAG CCG GGG CAA TCG CTT GAG 1428 30 TCG ACT GTC CAA ACA TGG TTT AAG CCG CTT GCT TAC GCT TTT ATT CTC 1476 ACA AGG GAA TCT GGA TAC CCT CAG GTT TTC TAC GGG GAT ATG TAC GGG 1524 ACG AAA GGA GAC TCC CAG CGC GAA ATT CCT GCC TTG AAA CAC AAA ATT 1572 GAA CCG ATC TTA AAA GCG AGA AAA CAG TAT GCG TAC GGA GCA CAG CAT 1620 GAT TAT TTC GAC CAT GAC ATT GTC GGC TGG ACA AGG GAA GGC GAC 166B 40 AGC TCG GTT GCA AAT TCA GGT TTG GCG GCA TTA ATA ACA GAC GGA CCC 1716 GGT GGG GCA AAG CGA ATG TAT GTC GGC CGG CAA AAC GCC GGT GAG ACA 1764 TGG CAT GAC ATT ACC GGA AAC CGT TCG GAG CCG GTT GTC ATC AAT TCG 1812 45 GAA GGC TGG GGA GAG TTT CAC GTA AAC GGC GGG TCG GTT TCA ATT TAT 1860 GTT CAA AGA TAG AAGAGCAGAG AGGACGGATT TCCTGAAGGA AATCCGTTTT 1912 50 TTTATTTT 1920

(2) INFORMATION FOR SEO ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1455 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii)Organism: Bacillus sp.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CATCATAATG GAACAAATGG TACTATGATG CAATATTTCG AATGGTATTT GCCAAATGAC 60 GGGAATCATT GGAACAGGTT GAGGGATGAC GCAGCTAACT TAAAGAGTAA AGGGATAACA 120



15. NOV. 1999 18:27

	GCTGTATGGA	TCCCACCTGC	ATGGAAGGGG	ACTTCCCAGA	ATGATGTAGG	TTATGGAGCC	180
5	TATGATTTAT	ATGATCTTGG	AGAGTTTAAC	CAGAAGGGGA	CGGTTCGTAC	AAAATATGGA	240
	ACACGCAACC	AGCTACAGGC	TGCGGTGACC	TCTTTAAAAA	ATAACGGCAT	TCAGGTATAT	300
	GGTGATGTCG	TCATGAATCA	TAAAGGTGGA	GCAGATGGTA	CGGAAATTGT	AAATGCGGTA	360
10	GAAGTGAATC	GGAGCAACCG	AAACCAGGAA	ACCTCAGGAG	AGTATCCAAT	AGAAGCGTGG	420
	ACAAAGTTTG	ATTTTCCTGG	AAGAGGAAAT	AACCATTCCA	GCTTTAAGTG	GCGCTGGTAT	480
	CATTTTGATG	GGACAGATTG	GGATCAGTCA	CGCCAGCTTC	AAAACAAAAT	ATATAAATTC	540
15	AGGGGAACAG	GCAAGGCCTG	GGACTGGGAA	GTCGATACAG	AGAATGGCAA	CTATGACTAT	600
	CTTATGTATG	CAGACGTGGA	TATGGATCAC	CCAGAAGTAA	TACATGAACT	TAGAAACTGG	660
20	GGAGTGTGGT	ATACGAATAC	ACTGAACCTT	GATGGATTTA	GAATAGATGC	AGTGAAACAT	720
	ATAAAATATA	GCTTTACGAG	AGATTGGCTT	ACACATGTGC	GTAACACCAC	AGGTAAACCA	780
	ATGTTTGCAG	TGGCTGAGTT	TTGGAAAAAT	GACCTTGGTG	CAATTGAAAA	CTATTTGAAT	840
25	AAAACAAGTT	GGAATCACTC	GGTGTTTGAT	GTTCCTCTCC	ACTATAATTT	GTACAATGCA	900
	TCTAATAGCG	GTGGTTATTA	TGATATGAGA	AATATTTAA	ATGGTTCTGT	GGTGCAAAAA	960
30	CATCCAACAC	ATGCCGTTAC	TTTTGTTGAT	AACCATGATT	CTCAGCCCGG	GGAAGCATTG	1020
- •	GAATCCTTTG	TTCAACAATG	GTTTAAACCA	CTTGCATATG	CATTGGTTCT	GACAAGGGAA	1080
	CAAGGTTATC	CTTCCGTATT	TTATGGGGAT	TACTACGGTA	TCCCAACCCA	TGGTGTTCCG	1140
35	GCTATGAAAT	CTAAAATAGA	CCCTCTTCTG	CAGGCACGTC	AAACTTTTGC	CTATGGTACG	1200
	CAGCATGATT	ACTTTGATCA	TCATGATATT	ATCGGTTGGA	CAAGAGAGGG	AAATAGCTCC	1260
40	CATCCAAATT	CAGGCCTTGC	CACCATTATG	TCAGATGGTC	CAGGTGGTAA	CAAATGGATG	1320
	TATGTGGGGA	AAAATAAAGC	GGGACAAGTT	TGGAGAGATA	TTACCGGAAA	TAGGACAGGC	1380
	ACCGTCACAA	TTAATGCAGA	CGGATGGGGT	AATTTCTCTG	TTAATGGAGG	GTCCGTTTCG	1440
45	GTTTGGGTGA	AGCAA					1455
50	(2) INFORMATION FOR SEQ ID NO: 14:     (i) SEQUENCE CHARACTERISTICS:     (A) LENGTH: 1455 base pairs     (B) TYPE: nucleic acid     (C) STRANDEDNESS: single     (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) Organism: Bacillus sp.						
55	(xi) SE	EQUENCE DESC	RIPTION: SE	Q ID NO: 14	::		
		GGACAAATGG					60
60	GGGAATCACT	GGAATAGATT .	AAGAGATGAT	GCTAGTAATC	TAAGAAATAG	AGGTATAACC	120
	GCTATTTGGA	TTCCGCCTGC	CTGGAAAGGG	ACTTCGCAAA	ATGATGT <b>G</b> GG	GTATGGAGCC	180
65	TATGATCTTT	ATGATTTAGG	GGAATTTAAT	CAAAAGGGGA	CGGTTCGTAC	TAAGTATGGG	240
	ACACGTAGTC	AATTGGAGTC	TGCCATCCAT	GCTTTAAAGA	ATAATGGCGT	TCAAGTTTAT	300
	GGGGATGTAG	TGATGAACCA	TAAAGGAGGA	GCTGATGCTA	CAGAAAACGT	TCTTGCTGTC	360

50

19

	GAGGTGAATC	CAAATAACCG	GAATCAAGAA	ATATCTGGGG	ACTACACAAT	TGAGGCTTGG	420
5	ACTAAGTTTG	ATTTTCCAGG	GAGGGGTAAT	ACATACTCAG	ACTTTAAATG	GCGTTGGTAT	480
	CATTTCGATG	GTGTAGATTG	GGATCAATCA	CGACAATTCC	AAAATCGTAT	CTACAAATTC	540
	CGAGGTGATG	GTAAGGCATG	GGATTGGGAA	GTAGATTCGG	AAAATGGAAA	TTATGATTAT	600
10	TTAATGTATG	CAGATGTAGA	TATGGATCAT	CCGGAGGTAG	TAAATGAGCT	TAGAAGATGG	660
	GGAGAATGGT	ATACAAATAC	ATTAAATCTT	GATGGATTTA	GGATCGATGC	GGTGAAGCAT	720
15	ATTAAATATA	GCTTTACACG	TGATTGGTTG	ACCCATGTAA	GAAACGCAAC	GGGAAAAGAA	780
	ATGTTTGCTG	TTGCTGAATT	TTGGAAAAAT	GATTTAGGTG	CCTTGGAGAA	CTATTTAAAT	840
	AAAACAAACT	GGAATCATTC	TGTCTTTGAT	GTCCCCCTTC	ATTATAATCT	TTATAACGCG	900
20	TCAAATAGTG	GAGGCAACTA	TGACATGGCA	AAACTTCTTA	ATGGAACGGT	TGTTCAAAAG	960
	CATCCAATGC	ATGCCGTAAC	TTTTGTGGAT	AATCACGATT	CTCAACCTGG	GGAATCATTA	1020
25	GAATCATTTG	TACAAGAATG	GTTTAAGCCA	CTTGCTTATG	CGCTTATTTT	AACAAGAGAA	1080
	CAAGGCTATC	CCTCTGTCTT	CTATGGTGAC	TACTATGGAA	TTCCAACACA	TAGTCTCCCA	1140
	GCAATGAAAG	CCAAGATTGA	TCCAATCTTA	GAGGCGCGTC	AAAATTTTGC	ATATGGAACA	1200
Э0	CAACATGATT	ATTTTGACCA	TCATAATATA	ATCGGATGGA	CACGTGAAGG	AAATACCACG	1260
	CATCCCAATT	CAGGACTTGC	GACTATCATG	TCGGATGGGC	CAGGGGGAGA	GAAATGGATG	1320
35	TACGTAGGGC	AAAATAAAGC	AGGTCAAGTT	TGGCATGACA	TAACTGGAAA	TAAACCAGGA	1380
	ACAGTTACGA	TCAATGCAGA	TGGATGGGCT	AATTTTTCAG	TAAATGGAGG	ATCTGTTTCC	1440
	ATTTGGGTGA	AACGA					1455

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(2) INFORMATION FOR SEQ ID NO: 15:
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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/ KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "RSERI"

(ix) FEATURE:

(A) NAME/KEY: misc-feature

LOCATION: 21-62 (B)

(D): OTHER INFORMATION: /Note= 1:97%A, 1%T, 1%C, 1%G

2:97%T, 1%A, 1%C, 1%G 3:97%C, 1%A, 1%T, 1%G 4:97%G, 1%A, 1%T, 1%C

74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCGTTTTGCC GGCCGACATA 3122343222 4333313344 60 4233423242 2122112433 43CAAACCTG AATT

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20

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(D) TOPOLOGY: linear
          MOLECULE TYPE: other nucleic acid
    (ii)
    (ix) FEATURE:
          (A) NAME/ KEY: misc-feature:
                  (B) OTHER INFORMATION:
                                             /desc = "RSERII"
 5
          (ix) FEATURE:
          (A) NAME/KEY: misc-feature
         LOCATION: 63-104
    (B)
    (D): OTHER INFORMATION: /Note=
                                           1:97%A, 1%T, 1%C, 1%G
                                           2:97%T, 1%A, 1%C, 1%G
3:97%C, 1%A, 1%T, 1%G
4:97%G, 1%A, 1%T, 1%C
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
    GCGTTTTGCC GGCCGACATA CATTCGCTTT GCCCCACCGG GTCCGTCTGT
   TATTAATGCC GC31113324 1122243113 3414324234 3322333224
    2331GCCGAC AATGTCATGG TG
                                                                       122
    (2) INFORMATION FOR SEQ ID NO: 17:
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single (D) TOPOLOGY: linear
    (ii)
          MOLECULE TYPE: other nucleic acid
25 (ix) FEATURE:
          (A) NAME/ KEY: misc-feature:
                  (B) OTHER INFORMATION:
                                             /desc = "RSERIII"
          (ix) FEATURE:
         (A) NAME/KEY: misc-feature
30 (B)
        LOCATION: 19-60
    (D): OTHER INFORMATION: /Note=
                                           1:97%A, 1%T, 1%C, 1%G
2:97%T, 1%A, 1%C, 1%G
                                           3:97%C, 1%A, 1%T, 1%G
                                           4:97%G, 1%A, 1%T, 1%C
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
   GTCGCCTTCC CTTGTCCA43 3413112423 1244244234 1112112312 4324243233 GTACGCATAC TGTTTTCT
                                                                            78
40 (2) INFORMATION FOR SEQ ID NO: 18:
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 20 base pairs(B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
45
    (ii)
          MOLECULE TYPE: other nucleic acid
    (ix) FEATURE:
         (A) NAME/ KEY: misc-feature:
                 (B) OTHER INFORMATION:
                                              /desc = "FSERIII"
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
    TGGACAAGGG AAGGCGACAG
                                                                            20
    (2) INFORMATION FOR SEQ ID NO: 19:
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
55
               (C) STRANDEDNESS: single (D) TOPOLOGY: linear
          MOLECULE TYPE: other nucleic acid
    (ii)
    (ix) FEATURE:
          (A) NAME/ KEY: misc-feature:
                  (B) OTHER INFORMATION:
                                               /desc = "RSERV"
          (ix) FEATURE:
         (A) NAME/KEY: misc-feature
         LOCATION: 19-60
    (B)
                                           1:97%A, 1%T, 1%C, 1%G
2:97%T, 1%A, 1%C, 1%G
    (D): OTHER INFORMATION: /Note=
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3:978C, 18A, 18T, 18G
4:978G, 18A, 18T, 18C
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
TAAGATCGGT TCAATTTT42 4222311443 1441122234 3432444142 3233222342 CCCGTACATA TCCCCGTAGA A
   (2) INFORMATION FOR SEQ ID NO: 20:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid
10
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
   (ii)
         MOLECULE TYPE: other nucleic acid
   (ix) FEATURE:
         (A) NAME/ KEY: misc-feature:
                (B) OTHER INFORMATION:
                                           /desc = "FSERV"
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                        18
   AAAATTGAAC CGATCTTA
   (2) INFORMATION FOR SEQ ID NO: 21:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 107 base pairs
              (B) TYPE: nucleic acid (C) STRANDEDNESS: single
25
              (D) TOPOLOGY: linear
         MOLECULE TYPE: other nucleic acid
   (ii)
   (ix) FEATURE:
         (A) NAME/ KEY: misc-feature:
                 (B) OTHER INFORMATION:
                                            /desc = "FSERVII"
         (ix) FEATURE:
         (A) NAME/KEY: misc-feature
        LOCATION: 54-95
   (B)
35 (D): OTHER INFORMATION: /Note=
                                        1:97%A, 1%T, 1%C, 1%G
                                        2:97%T, 1%A, 1%C, 1%G
                                        3:97%C, 1%A, 1%T, 1%G
4:97%G, 1%A, 1%T, 1%C
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
GAA3442134 4234222331 1431233422 4111234422 13122TGTCG
   ATAACCA
                                                                        108
  (2) INFORMATION FOR SEQ ID NO: 22:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 18 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
50
   (ii) MOLECULE TYPE: other nucleic acid
   (ix) FEATURE:
         (A) NAME/ KEY: misc-feature:
                (B) OTHER INFORMATION:
                                            /desc = "RSERVII"
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
   TGTCGATGCA GCATGGAA
                                                                        19
   (2) INFORMATION FOR SEQ ID NO: 23:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 80 base pairs (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
65 (ii) MOLECULE TYPE: other nucleic acid
   (ix) FEATURE:
         (A) NAME/ KEY: misc-feature:
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(B) OTHER INFORMATION:
                                           /desc = "FSERIX"
         (ix) FEATURE:
         (A) NAME/KEY: misc-feature
        LOCATION: 21-62
  (D): OTHER INFORMATION: /Note=
                                        1:978A, 18T, 18C, 18G
                                        2:97%T, 1%A, 1%C, 1%G
3:97%C, 1%A, 1%T, 1%G
                                        4:978G, 1%A, 1%T, 1%C
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
10 GTCCAAACAT GGTTTAAGCC 4322432213 4322221223 2313114441
   1232441213 33TCAGGTTT TCTACGGGGA
                                                                  80
   (2) INFORMATION FOR SEQ ID NO: 24:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 20 base pairs
15
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
         MOLECULE TYPE: other nucleic acid
   (ii)
20 (ix) FEATURE:
         (A) NAME/ KEY: misc-feature:
                                          /desc = "RSERIX"
                (B) OTHER INFORMATION:
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
   GGCTTAAACC ATGTTTGGAC
   (2) INFORMATION FOR SEQ ID NO: 26:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 24 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: other nucleic acid
   (ix) FEATURE:
         (A) NAME/ KEY: misc-feature:
                (B) OTHER INFORMATION: /desc = "Primer 1B"
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                  24
   CGATTGCTGA CGCTGTTATT TGCG
   (2) INFORMATION FOR SEQ ID NO: 27: (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 25 base pairs
              (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
  (ii)
         MOLECULE TYPE: other nucleic acid
   (ix) FEATURE:
         (A) NAME/ KEY: misc-feature:
                (B) OTHER INFORMATION:
                                          /desc = "Primer #63"
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
50 CTATCTTTGA ACATAAATTG AAACC
                                                                  25
   (2) INFORMATION FOR SEQ ID NO: 28:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 20 base pairs
55
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: other nucleic acid
   (ix) FEATURE:
         (A) NAME/ KEY: misc-feature:
                (B) OTHER INFORMATION: /desc = "forward Primerl"
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
   gacctgcagt caggcaacta
    (2) INFORMATION FOR SEQ ID NO: 29:
         (i) SEQUENCE CHARACTERISTICS:
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	(A) LENGTH: 20 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: other nucleic acid (ix) PEATURE:	
	<pre>(A) NAME/ KEY: misc-feature:     (B) OTHER INFORMATION: /desc = "reverse primer 1"</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:	
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	(2) INFORMATION FOR SEQ ID NO: 30:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid	
	(ix) FEATURE:	
20	<pre>(A) NAME/ KEY: misc-feature:</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:	
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25	(2) INFORMATION FOR SEQ ID NO: 31:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
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35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:	
	tagagtegae etgeaggeat 20	
	(a) Typopyamrov Bon and The No. 10	
40	(2) INFORMATION FOR SEQ ID NO: 32: (i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2084 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	<pre>(ii) MOLECULE TYPE: DNA (genomic) (iii)Organism: Bacillus amyloliquefaciens</pre>	
	(ix) FEATURE:	
	(A) NAME/KEY: CDS (B) LOCATION: 3431794	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:	
	GCCCCGCACA TACGAAAAGA CTGGCTGAAA ACATTGAGCC TTTGATGACT GATGATTTGG	60
		00
55	CTGAAGAAGT GGATCGATTG TTTGAGAAAA GAAGAAGACC ATAAAAATAC CTTGTCTGTC	120
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	ACGCTGTTAT TTGTCAGTTT GCCGATTACA AAAACATCAG CC GTA AAT GGC ACG	354
65	CTG ATG CAG TAT TTT GAA TGG TAT ACG CCG AAC GAC GGC CAG CAT TGG	402
	AAA CGA TTG CAG AAT GAT GCG GAA CAT TTA TCG GAT ATC GGA ATC ACT	450



GCC GTQ TGG ATT CCT CCC GCA TAC AAA GGA TTG AGC CAA TCC GAT AAC 49B GGA TAC GGA CCT TAT GAT TTG TAT GAT TTA GGA GAA TTC CAG CAA AAA 5 GGG ACG GTC AGA ACG AAA TAC GGC ACA AAA TCA GAG CTT CAA GAT GCG 594 ATC GGC TCA CTG CAT TCC CGG AAC GTC CAA GTA TAC GGA GAT GTG GTT 642 TTG AAT CAT AAG GCT GGT GCT GAT GCA ACA GAA GAT GTA ACT GCC GTC 690 GAA GTC AAT CTG GCC AAT AGA AAT CAG GAA ACT TCG GAG GAA TAT CAA 738 ATC AAA GCG TGG ACG GAT TTT CGT TTT CCG GGC CGT GGA AAC ACG TAC 786 15 AGT GAT TIT AAA TGG CAT TGG TAT CAT TTC GAC GGA GCG GAC TGG GAT gaa too ogg aag ato ago ogc ato tit aag tit ogt ggg gaa gga aaa 882 GCG TGG GAT TGG GAA GTA TCA AGT GAA AAC GGC AAC TAT GAC TAT TTA 930 ATG TAT GCT GAT GTT GAC TAC GAC CAC CCT GAT GTC GTG GCA GAG ACA 978 AAA AAA TGG GGT ATC TGG TAT GCG AAT GAA CTG TCA TTA GAC GGC TTC 1026 25 CGT ATT GAT GCC GCC AAA\CAT ATT AAA ITT TCA TTT CTG CGT GAT TGG 1074 GTT CAG GCG GTC AGA CAG GCG ACG GGA AAA GAA ATG TTT ACG GTT GCG 1122 GAG TAT TGG CAG AAT AAT GCC GGG AAA CTC GAA AAC TAC TTG AAT AAA 1170 ACA AGC TTT AAT CAA TCC GTG\TTT GAT GTT CCG CTT CAT TTC AAT TTA 1218 CAG GCG GCT TCC TCA CAA GGA GGC GGA TAT GAT ATG AGG CGT TTG CTG 1266 35 GAC GGT ACC GTT GTG TCC AGG CAT CCG GAA AAG GCG GTT ACA TTT GTT 1314 GAA AAT CAT GAC ACA CAG CCG GGA\CAG TCA TTG GAA TCG ACA GTC CAA 1362 act tgg ttt aaa ccg ctt gca tac gcc ttt att ttg aca aga gaa tcc 1410 GGT TAT CCT CAG GTG TIC TAT GGG GAT ATG TAC GGG ACA AAA GGG ACA 1458 TCG CCA AAG GAA ATT CCC TCA CTG AAA\GAT AAT ATA GAG CCG ATT TTA 1506 45 AAA GCG CGT AAG GAG TAC GCA TAC GGG CCC CAG CAC GAT TAT ATT GAC 1554 CAC CCG GAT GTG ATC GGA TGG ACG AGG GAA GGT GAC AGC TCC GCC GCC 1602 aaa toa ggt tig god got tia ato aog gad gga coo ggo gga toa aag 1650 CGG ATG TAT GCC GGC CTG AAA AAT GCC GGC GAG ACA TGG TAT GAC ATA 1698 ACG GGC AAC CGT TCA GAT ACT GTA AAA ATC GOA TCT GAC GGC TGG GGA 1746 55 GAG TTT CAT GTA AAC GAT GGG TCC GTC TCC ATT TAT GTT CAG AAA TAA 1794 GGTAATAAAA AAACACCTCC AAGCTGAGTG CGGGTATCAG CTTGGAGGTG CGTTTATTTT 1854 TTCAGCCGTA TGACAAGGTC GGCATCAGGT GTGACAAATA CGGTATGCTG GCTGTCATAG 1914 GTGACAAATC CGGGTTTTGC GCCGTTTGGC TTTTTCACAT GTGTGATTTT TGTATAATCA 1974 ACAGGCACGG AGCCGGAATC TTTCGCCTTG GAAAAATAAG CGGGGATCGT AGCTGCTTCC 2034 65 AATATGGATT GTTCATCGGG ATCGCTGCTT TTAATCACAA CGTGGGATCC 2084